

**AMENDMENTS TO THE CLAIMS:**

This listing of claims will replace all prior versions and listings of claims in the application:

1 - 5. (Canceled)

6. (Currently amended) The method of claim 8, wherein the DNA methylation pattern for the test stem cell, test stem cell tissue, or test stem cell nucleus and the differentiation state-specific DNA methylation pattern each comprise information on the methylation state of at least about 1,000 gene regions.

7. (Canceled)

8. (Currently amended) A method of identifying the differentiation state of a test stem cell, test stem cell tissue, or test stem cell nucleus comprising:

obtaining a DNA methylation pattern for the test stem cell, test stem cell tissue, or test stem cell nucleus, wherein the DNA methylation pattern for the test stem cell, test stem cell tissue, or test stem cell nucleus comprises information on the methylation state of CpG at a plurality of gene regions;

obtaining a differentiation state-specific DNA methylation pattern for one or more stem cell, stem cell tissue, or stem cell nucleus of known differentiation state; and,

comparing the DNA methylation pattern for the test stem cell, test stem cell tissue, or test stem cell nucleus with the differentiation state-specific DNA methylation pattern,

wherein the differentiation state of the test stem cell, test stem cell tissue, or test stem cell nucleus is identified if the DNA methylation pattern of the test stem cell, test stem cell tissue, or test stem cell nucleus matches the differentiation state-specific DNA methylation pattern.

9. (Previously presented) The method of claim 8, wherein the DNA methylation patterns are obtained by generating RLGS profiles.

10 - 18. (Canceled)

19. (Currently amended) The method of claim 8, wherein the test stem cell, test stem cell tissue, or test stem cell nucleus is an embryonic stem cell, embryonic stem cell tissue, or embryonic stem cell nucleus.

20. (Currently amended) The method of claim 8, wherein the differentiation state of the one or more stem cell, stem cell tissue, or stem cell nucleus of known differentiation state is differentiated.

21. (Currently amended) The method of claim 8, wherein the differentiation state of the one or more stem cell, stem cell tissue, or stem cell nucleus of known differentiation state is undifferentiated.

22. (Currently amended) A method of identifying a test stem cell, test stem cell tissue, or test stem cell nucleus, comprising:

obtaining a DNA methylation pattern for the test stem cell, test stem cell tissue, or test stem cell nucleus, wherein the DNA methylation pattern for the test stem cell, test stem cell tissue, or test stem cell nucleus comprises information on the methylation state of CpG at a plurality of gene regions;

obtaining a cell-, tissue-, or nucleus-specific DNA methylation pattern for one or more known types of stem cell, stem cell tissue, or stem cell nucleus; wherein the one or more known types of stem cell, stem cell tissue, or stem cell nucleus is selected from undifferentiated embryonic stem cell, differentiated embryonic stem cell, undifferentiated trophoblast stem cell, and differentiated trophoblast stem cell; and,

comparing the DNA methylation pattern for the test stem cell, test stem cell tissue, or test stem cell nucleus with the cell-, tissue-, or nucleus-specific DNA methylation pattern of the known stem cell,

stem cell tissue, or stem cell nucleus to permit identification of the test stem cell, test stem cell tissue, or test stem cell nucleus as one of the known types of stem cell, stem cell tissue, or stem cell nucleus;

wherein a match to the cell-, tissue-, or nucleus-specific DNA methylation pattern of the undifferentiated embryonic stem cell identifies the test stem cell, test stem cell tissue, or test stem cell nucleus as undifferentiated embryonic stem cell;

wherein a match to the cell-, tissue-, or nucleus-specific DNA methylation pattern of the differentiated embryonic stem cell identifies the test stem cell, test stem cell tissue, or test stem cell nucleus as differentiated embryonic stem cell;

wherein a match to the cell-, tissue-, or nucleus-specific DNA methylation pattern of the undifferentiated trophoblast stem cell identifies the test stem cell, test stem cell tissue, or test stem cell nucleus as undifferentiated trophoblast stem cell;

wherein a match to the cell-, tissue-, or nucleus-specific DNA methylation pattern of the differentiated trophoblast stem cell identifies the test stem cell, test stem cell tissue, or test stem cell nucleus as differentiated trophoblast stem cell.

23. (Previously presented) The method of claim 22, wherein the DNA methylation patterns are obtained by generating RLGS profiles.